

## RAW SEQUENCE LISTING

DATE: 08/13/2001

PATENT APPLICATION: US/09/532,263

TIME: 11:08:17

Input Set : N:\Crf3\RULE60\09532263.txt

Output Set: N:\CRF3\08132001\I532263.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hilton, Douglas J.

7 (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

9 (iii) NUMBER OF SEQUENCES: 25

11 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

14 (B) STREET: 400 Garden City Plaza

15 (C) CITY: Garden City

16 (D) STATE: New York

17 (E) COUNTRY: United States of America

18 (F) ZIP: 11530

20 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/532,263

C--> 30 (B) FILING DATE: 22-Apr-2000

31 (C) CLASSIFICATION:

C--> 35 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/702,665

38 (B) FILING DATE:

43 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Presser, Leopold

46 (B) REGISTRATION NUMBER: 19,827

47 (C) REFERENCE/DOCKET NUMBER: 10296

49 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: (516) 742-4343

52 (B) TELEFAX: (516) 742-4366

53 (C) TELEX: 203 901 SANS UR

55 (2) INFORMATION FOR SEQ ID NO: 1:

57 (i) SEQUENCE CHARACTERISTICS:

59 (A) LENGTH: 5 amino acids

60 (B) TYPE: amino acid

61 (C) STRANDEDNESS: single

62 (D) TOPOLOGY: linear

W--> 64 (ii) MOLECULE TYPE:

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 68 Trp Ser Xaa Trp Ser

69 1 5

71 (2) INFORMATION FOR SEQ ID NO: 2:

73 (i) SEQUENCE CHARACTERISTICS:

75 (A) LENGTH: 1705 base pairs

76 (B) TYPE: nucleic acid

77 (C) STRANDEDNESS: single

ENTERED

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78      (D) TOPOLOGY: linear
80      (ii) MOLECULE TYPE: DNA (genomic)
82      (ix) FEATURE:
84          (A) NAME/KEY: CDS
85          (B) LOCATION: 45..1340
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
89 GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC      56
90                                     Met Ser Ser Ser
91                                     1
93 TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG      104
94 Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val
95   5          10          15          20
97 TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG      152
98 Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln
99          25          30          35
101 TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT      200
102 Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser
103          40          45          50
105 GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC      248
106 Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu
107          55          60          65
109 CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG      296
110 Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val
111          70          75          80
113 GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA      344
114 Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val
115          85          90          95          100
117 TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT      392
118 Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro
119          105          110          115
121 GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG      440
122 Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp
123          120          125          130
125 AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC      488
126 Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr
127          135          140          145
129 AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC      536
130 Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser
131          150          155          160
133 ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT      584
134 Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys
135          165          170          175          180
137 GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC      632
138 Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr
139          185          190          195
141 GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA      680
142 Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu
143          200          205          210
145 CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC      728

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146 Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser
147      215      220      225
149 GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC      776
150 Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala
151      230      235      240
153 TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC      824
154 Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr
155 245      250      255      260
157 CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG      872
158 Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu
159      265      270      275
161 GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA      920
162 Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg
163      280      285      290
165 GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC      968
166 Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser
167      295      300      305
169 CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA      1016
170 Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile
171      310      315      320
173 CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT      1064
174 Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala
175 325      330      335      340
176 CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA      1112
177 Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro
178      345      350      355
180 AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG      1160
181 Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala
182      360      365      370
184 TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA      1208
185 Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala
186      375      380      385
188 CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA      1256
189 Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln
190      390      395      400
192 AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA      1304
193 Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly
194 405      410      415      420
196 ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTTCATC      1350
197 Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
198      425      430
200 TGTAACCCGG TCAGACTGGG GGCAGAAAGA GGCAGGGGCG TGGATCCCTG TGGATGGAGG      1410
202 TCTCAGCTGA AAGTCTGAGC TCTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT      1470
204 GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA      1530
206 AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT      1590
208 GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA      1650
210 GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAA      1705
212 (2) INFORMATION FOR SEQ ID NO: 3:
214      (i) SEQUENCE CHARACTERISTICS:

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216      (A) LENGTH: 432 amino acids
217      (B) TYPE: amino acid
218      (D) TOPOLOGY: linear
220      (ii) MOLECULE TYPE: protein
222      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
224 Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala
225   1      5      10      15
227 Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
228      20      25      30
230 Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys
231      35      40      45
233 Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp
234      50      55      60
236 Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val
237      65      70      75      80
239 Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr
240      85      90      95
242 Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
243      100     105     110
245 Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
246      115     120     125
248 Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
249      130     135     140
251 Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
252 145      150     155     160
254 Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
255      165     170     175
257 Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
258      180     185     190
260 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
261      195     200     205
263 Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
264      210     215     220
266 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp
267 225      230     235     240
269 Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe
270      245     250     255
272 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
273      260     265     270
275 Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
276      275     280     285
278 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
279      290     295     300
281 Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu
282 305      310     315     320
285 Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu
286      325     330     335
288 Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu
289      340     345     350

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291 Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val
292          355          360          365
294 Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val
295          370          375          380
297 Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys
298 385          390          395          400
300 Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu
301          405          410          415
303 Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
304          420          425          430
306 (2) INFORMATION FOR SEQ ID NO: 4:
308 (i) SEQUENCE CHARACTERISTICS:
310 (A) LENGTH: 1800 base pairs
311 (B) TYPE: nucleic acid
312 (C) STRANDEDNESS: single
313 (D) TOPOLOGY: linear
315 (ii) MOLECULE TYPE: cDNA
317 (ix) FEATURE:
319 (A) NAME/KEY: CDS
320 (B) LOCATION: 128..1396
322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
324 TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTCTCC TAGGAAGCCT CAGTTTGGGA      60
326 GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTGGAC TCTACCTCTC      120
328 CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC      169
329 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala
W--> 330          435          440          445
332 GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG      217
333 Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp
W--> 334          450          455          460
336 GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG      265
337 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu
W--> 338          465          470          475
340 TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT      313
341 Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp
W--> 342          480          485          490
344 GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA      361
345 Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu
W--> 346 495          500          505          510
348 CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC      409
349 Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys
W--> 350          515          520          525
352 CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC      457
353 Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly
W--> 354          530          535          540
356 TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG      505
357 Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu
W--> 358          545          550          555
360 AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC      553
361 Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr

```

## VERIFICATION SUMMARY

DATE: 08/13/2001

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TIME: 11:08:18

Input Set : N:\Cr3\RULE60\09532263.txt

Output Set: N:\CRF3\08132001\I532263.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:64 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1  
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:394 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:401 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4